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List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

108
papers

19,974
citations

40
h-index

129
g-index

129
ext. papers

30,038
ext. citations

9.1
avg, IF

6.98
L-index

#	Paper	IF	Citations
108	A transcriptomic dataset evaluating the effect of radiotherapy injury on cells of skin and soft tissue.. <i>Data in Brief</i> , 2022 , 41, 107828	1.2	1
107	BAF complex-mediated chromatin relaxation is required for establishment of X chromosome inactivation.. <i>Nature Communications</i> , 2022 , 13, 1658	17.4	0
106	Dashboard-style interactive plots for RNA-seq analysis are R Markdown ready with 2.0.. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab116	3.7	0
105	Benchmarking UMI-based single-cell RNA-seq preprocessing workflows.. <i>Genome Biology</i> , 2021 , 22, 339	18.3	5
104	Comprehensive characterization of single-cell full-length isoforms in human and mouse with long-read sequencing. <i>Genome Biology</i> , 2021 , 22, 310	18.3	10
103	NanoMethViz: An R/Bioconductor package for visualizing long-read methylation data. <i>PLoS Computational Biology</i> , 2021 , 17, e1009524	5	3
102	The impact of influenza pulmonary infection and inflammation on vagal bronchopulmonary sensory neurons. <i>FASEB Journal</i> , 2021 , 35, e21320	0.9	6
101	Single-cell analyses reveal the clonal and molecular aetiology of Flt3L-induced emergency dendritic cell development. <i>Nature Cell Biology</i> , 2021 , 23, 219-231	23.4	7
100	The long and the short of it: unlocking nanopore long-read RNA sequencing data with short-read differential expression analysis tools. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab028	3.7	8
99	Clonal multi-omics reveals Bcor as a negative regulator of emergency dendritic cell development. <i>Immunity</i> , 2021 , 54, 1338-1351.e9	32.3	5
98	Homeostatic apoptosis prevents competition-induced atrophy in follicular B cells. <i>Cell Reports</i> , 2021 , 36, 109430	10.6	1
97	long-read-tools.org: an interactive catalogue of analysis methods for long-read sequencing data. <i>GigaScience</i> , 2021 , 10,	7.6	3
96	Single-Cell Transcriptomic Analysis Reveals BCMA CAR-T Cell Dynamics in a Patient with Refractory Primary Plasma Cell Leukemia. <i>Molecular Therapy</i> , 2021 , 29, 645-657	11.7	10
95	Community-wide hackathons to identify central themes in single-cell multi-omics. <i>Genome Biology</i> , 2021 , 22, 220	18.3	2
94	Modulation of Vagal Sensory Neurons High Mobility Group Box-1 and Receptor for Advanced Glycation End Products: Implications for Respiratory Viral Infections. <i>Frontiers in Physiology</i> , 2021 , 12, 744812	4.6	2
93	Unique properties of a subset of human pluripotent stem cells with high capacity for self-renewal. <i>Nature Communications</i> , 2020 , 11, 2420	17.4	13
92	Harnessing Natural Killer Immunity in Metastatic SCLC. <i>Journal of Thoracic Oncology</i> , 2020 , 15, 1507-1528.	8.9	23

91	The EMT modulator SNAI1 contributes to AML pathogenesis via its interaction with LSD1. <i>Blood</i> , 2020 , 136, 957-973	2.2	12
90	Opportunities and challenges in long-read sequencing data analysis. <i>Genome Biology</i> , 2020 , 21, 30	18.3	431
89	Targeting triple-negative breast cancers with the Smac-mimetic birinapant. <i>Cell Death and Differentiation</i> , 2020 , 27, 2768-2780	12.7	13
88	is a maternal effect gene required for genomic imprinting. <i>ELife</i> , 2020 , 9,	8.9	4
87	A guide to creating design matrices for gene expression experiments. <i>F1000Research</i> , 2020 , 9, 1444	3.6	3
86	The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity. <i>Nature Immunology</i> , 2020 , 21, 168-177	19.1	74
85	CellBench: R/Bioconductor software for comparing single-cell RNA-seq analysis methods. <i>Bioinformatics</i> , 2020 , 36, 2288-2290	7.2	15
84	Covering all your bases: incorporating intron signal from RNA-seq data. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa073	3.7	7
83	A new lymphoid-primed progenitor marked by Dach1 downregulation identified with single cell multi-omics. <i>Nature Immunology</i> , 2020 , 21, 1574-1584	19.1	4
82	Transcriptional Profiling of Individual Airway Projecting Vagal Sensory Neurons. <i>Molecular Neurobiology</i> , 2020 , 57, 949-963	6.2	29
81	Germline heterozygous mutations in Nxf1 perturb RNA metabolism and trigger thrombocytopenia and lymphopenia in mice. <i>Blood Advances</i> , 2020 , 4, 1270-1283	7.8	4
80	Distinct initiating events underpin the immune and metabolic heterogeneity of KRAS-mutant lung adenocarcinoma. <i>Nature Communications</i> , 2019 , 10, 4190	17.4	37
79	Benchmarking single cell RNA-sequencing analysis pipelines using mixture control experiments. <i>Nature Methods</i> , 2019 , 16, 479-487	21.6	135
78	Using long-read sequencing to detect imprinted DNA methylation. <i>Nucleic Acids Research</i> , 2019 , 47, e46	20.1	55
77	Interconversion between Tumorigenic and Differentiated States in Acute Myeloid Leukemia. <i>Cell Stem Cell</i> , 2019 , 25, 258-272.e9	18	32
76	BiocPkgTools: Toolkit for mining the package ecosystem. <i>F1000Research</i> , 2019 , 8, 752	3.6	
75	Synergy between the KEAP1/NRF2 and PI3K Pathways Drives Non-Small-Cell Lung Cancer with an Altered Immune Microenvironment. <i>Cell Metabolism</i> , 2018 , 27, 935-943.e4	24.6	106
74	Identification of a Siglec-F+ granulocyte-macrophage progenitor. <i>Journal of Leukocyte Biology</i> , 2018 , 104, 123-133	6.5	7

73	Smchd1 regulates long-range chromatin interactions on the inactive X chromosome and at Hox clusters. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 766-777	17.6	47
72	scPipe: A flexible R/Bioconductor preprocessing pipeline for single-cell RNA-sequencing data. <i>PLoS Computational Biology</i> , 2018 , 14, e1006361	5	59
71	Lung morphogenesis is orchestrated through Grainyhead-like 2 (Grhl2) transcriptional programs. <i>Developmental Biology</i> , 2018 , 443, 1-9	3.1	8
70	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. <i>Nucleic Acids Research</i> , 2017 , 45, e30	20.1	19
69	Identification of quiescent and spatially restricted mammary stem cells that are hormone responsive. <i>Nature Cell Biology</i> , 2017 , 19, 164-176	23.4	72
68	Cisplatin Increases Sensitivity to FGFR Inhibition in Patient-Derived Xenograft Models of Lung Squamous Cell Carcinoma. <i>Molecular Cancer Therapeutics</i> , 2017 , 16, 1610-1622	6.1	16
67	Thymospheres Are Formed by Mesenchymal Cells with the Potential to Generate Adipocytes, but Not Epithelial Cells. <i>Cell Reports</i> , 2017 , 21, 934-942	10.6	14
66	High-LET Radiation Increases Tumor Progression in a K-Ras-Driven Model of Lung Adenocarcinoma. <i>Radiation Research</i> , 2017 , 188, 562-570	3.1	3
65	Easy and efficient ensemble gene set testing with EGSEA. <i>F1000Research</i> , 2017 , 6, 2010	3.6	29
64	Glimma: interactive graphics for gene expression analysis. <i>Bioinformatics</i> , 2017 , 33, 2050-2052	7.2	65
63	Combining multiple tools outperforms individual methods in gene set enrichment analyses. <i>Bioinformatics</i> , 2017 , 33, 414-424	7.2	64
62	Loss of PUMA (BBC3) does not prevent thrombocytopenia caused by the loss of BCL-XL (BCL2L1). <i>British Journal of Haematology</i> , 2016 , 174, 962-9	4.5	6
61	Setdb1-mediated H3K9 methylation is enriched on the inactive X and plays a role in its epigenetic silencing. <i>Epigenetics and Chromatin</i> , 2016 , 9, 16	5.8	42
60	Transcriptional profiling of the epigenetic regulator Smchd1. <i>Genomics Data</i> , 2016 , 7, 144-7		9
59	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , 2016 , 5, 1408	3.6	250
58	The Transcription Factor PU.1 Controls a Reversible Differentiation Program in Acute Myeloid Leukemia. <i>Blood</i> , 2016 , 128, 3930-3930	2.2	
57	Uncovering Key Downstream Effectors of PU.1 Tumor Suppression in Acute Myeloid Leukemia. <i>Blood</i> , 2016 , 128, 2698-2698	2.2	
56	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , 2016 , 5, 1408	3.6	81

55	Deciphering the Innate Lymphoid Cell Transcriptional Program. <i>Cell Reports</i> , 2016 , 17, 436-447	10.6	89
54	High concordance between Illumina HiSeq2500 and NextSeq500 for reduced representation bisulfite sequencing (RRBS). <i>Genomics Data</i> , 2016 , 10, 97-100		8
53	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , 2016 , 5, 1408	3.6	213
52	A pooled shRNA screen for regulators of primary mammary stem and progenitor cells identifies roles for Asap1 and Prox1. <i>BMC Cancer</i> , 2015 , 15, 221	4.8	25
51	Repression of Igf1 expression by Ezh2 prevents basal cell differentiation in the developing lung. <i>Development (Cambridge)</i> , 2015 , 142, 1458-69	6.6	39
50	Why weight? Modelling sample and observational level variability improves power in RNA-seq analyses. <i>Nucleic Acids Research</i> , 2015 , 43, e97	20.1	227
49	Transcriptome and H3K27 tri-methylation profiling of Ezh2-deficient lung epithelium. <i>Genomics Data</i> , 2015 , 5, 346-51		2
48	Genome-wide binding and mechanistic analyses of Smchd1-mediated epigenetic regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E3535-44	11.5	63
47	limma powers differential expression analyses for RNA-sequencing and microarray studies. <i>Nucleic Acids Research</i> , 2015 , 43, e47	20.1	13379
46	Laparoscopic adjustable gastric banding and progression from impaired fasting glucose to diabetes. <i>Diabetologia</i> , 2014 , 57, 463-8	10.3	16
45	KRLMM: an adaptive genotype calling method for common and low frequency variants. <i>BMC Bioinformatics</i> , 2014 , 15, 158	3.6	3
44	197. <i>Cytokine</i> , 2014 , 70, 75-76	4	
43	Multidisciplinary diabetes care with and without bariatric surgery in overweight people: a randomised controlled trial. <i>Lancet Diabetes and Endocrinology,the</i> , 2014 , 2, 545-52	18.1	94
42	shRNA-seq data analysis with edgeR. <i>F1000Research</i> , 2014 , 3, 95	3.6	58
41	Apoptotic caspases suppress mtDNA-induced STING-mediated type I IFN production. <i>Cell</i> , 2014 , 159, 1549-62	56.2	475
40	Global changes in the mammary epigenome are induced by hormonal cues and coordinated by Ezh2. <i>Cell Reports</i> , 2013 , 3, 411-26	10.6	96
39	Targeting BCL-2 with the BH3 mimetic ABT-199 in estrogen receptor-positive breast cancer. <i>Cancer Cell</i> , 2013 , 24, 120-9	24.3	211
38	illuminaio: An open source IDAT parsing tool for Illumina microarrays. <i>F1000Research</i> , 2013 , 2, 264	3.6	47

37	Allele-specific expression analysis methods for high-density SNP microarray data. <i>Bioinformatics</i> , 2012 , 28, 1102-8	7.2	8
36	Sensitization of BCL-2-expressing breast tumors to chemotherapy by the BH3 mimetic ABT-737. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 2766-71	11.5	156
35	Comparing genotyping algorithms for Illumina's Infinium whole-genome SNP BeadChips. <i>BMC Bioinformatics</i> , 2011 , 12, 68	3.6	33
34	BeadArray expression analysis using bioconductor. <i>PLoS Computational Biology</i> , 2011 , 7, e1002276	5	45
33	Using the R Package crlmm for Genotyping and Copy Number Estimation. <i>Journal of Statistical Software</i> , 2011 , 40, 1-32	7.3	445
32	Using the R Package crlmm for Genotyping and Copy Number Estimation. <i>Journal of Statistical Software</i> , 2011 , 40,	7.3	40
31	Gene network disruptions and neurogenesis defects in the adult Ts1Cje mouse model of Down syndrome. <i>PLoS ONE</i> , 2010 , 5, e11561	3.7	34
30	A re-annotation pipeline for Illumina BeadArrays: improving the interpretation of gene expression data. <i>Nucleic Acids Research</i> , 2010 , 38, e17	20.1	185
29	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. <i>Genome Biology</i> , 2010 , 11, R24	18.3	81
28	Opposing roles of polycomb repressive complexes in hematopoietic stem and progenitor cells. <i>Blood</i> , 2010 , 116, 731-9	2.2	104
27	Data analysis issues for allele-specific expression using Illumina's GoldenGate assay. <i>BMC Bioinformatics</i> , 2010 , 11, 280	3.6	4
26	High-throughput analysis of candidate imprinted genes and allele-specific gene expression in the human term placenta. <i>BMC Genetics</i> , 2010 , 11, 25	2.6	51
25	Considerations for the processing and analysis of GoldenGate-based two-colour Illumina platforms. <i>Statistical Methods in Medical Research</i> , 2009 , 18, 437-52	2.3	17
24	Microarray background correction: maximum likelihood estimation for the normal-exponential convolution. <i>Biostatistics</i> , 2009 , 10, 352-63	3.7	120
23	R/Bioconductor software for Illumina's Infinium whole-genome genotyping BeadChips. <i>Bioinformatics</i> , 2009 , 25, 2621-3	7.2	43
22	Illumina WG-6 BeadChip strips should be normalized separately. <i>BMC Bioinformatics</i> , 2009 , 10, 372	3.6	19
21	Statistical issues in the analysis of Illumina data. <i>BMC Bioinformatics</i> , 2008 , 9, 85	3.6	82
20	Integrative analysis of RUNX1 downstream pathways and target genes. <i>BMC Genomics</i> , 2008 , 9, 363	4.5	93

19	Spike-in validation of an Illumina-specific variance-stabilizing transformation. <i>BMC Research Notes</i> , 2008 , 1, 18	2.3	13
18	Functional and metabolic remodelling in GLUT4-deficient hearts confers hyper-responsiveness to substrate intervention. <i>Journal of Molecular and Cellular Cardiology</i> , 2008 , 44, 270-80	5.8	40
17	Modifier effects between regulatory and protein-coding variation. <i>PLoS Genetics</i> , 2008 , 4, e1000244	6	30
16	Myocardial gene expression associated with genetic cardiac hypertrophy in the absence of hypertension. <i>Hypertension Research</i> , 2008 , 31, 941-55	4.7	8
15	beadarray: R classes and methods for Illumina bead-based data. <i>Bioinformatics</i> , 2007 , 23, 2183-4	7.2	398
14	A comparison of background correction methods for two-colour microarrays. <i>Bioinformatics</i> , 2007 , 23, 2700-7	7.2	741
13	Empirical array quality weights in the analysis of microarray data. <i>BMC Bioinformatics</i> , 2006 , 7, 261	3.6	222
12	Gene expression changes during step-wise differentiation of embryonic stem cells along the inner ear hair cell pathway. <i>Acta Oto-Laryngologica</i> , 2006 , 126, 1148-57	1.6	9
11	The long and the short of it: unlocking nanopore long-read RNA sequencing data with short-read tools		1
10	Combining multiple tools outperforms individual methods in gene set enrichment analyses		4
9	scPipe: a flexible R/Bioconductor preprocessing pipeline for single-cell RNA-sequencing data		7
8	Comprehensive characterization of single cell full-length isoforms in human and mouse with long-read sequencing		10
7	Long-range chromatin interactions on the inactive X and at Hox clusters are regulated by the non-canonical SMC protein Smchd1		3
6	Covering all your bases: incorporating intron signal from RNA-seq data		2
5	SIS-seq, a molecular time machine connects single cell fate with gene programs		3
4	scRNA-seq mixology: towards better benchmarking of single cell RNA-seq analysis methods		12
3	Using long-read sequencing to detect imprinted DNA methylation		5
2	Xmas ESC: A new female embryonic stem cell system that reveals the BAF complex as a key regulator of the establishment of X chromosome inactivation		1

1 NanoMethViz: an R/Bioconductor package for visualizing long-read methylation data

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